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Multimodal Connectivity of Motor Learning-Related Dorsal Premotor Cortex

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Abstract

The dorsal premotor cortex (dPMC) is a key region for motor learning and sensorimotor integration, yet we have limited understanding of its functional interactions with other regions. Previous work has started to examine functional connectivity in several brain areas using resting state functional connectivity (RSFC) and meta-analytical connectivity modelling (MACM). More recently, structural covariance (SC) has also been proposed as a technique that may also allow delineation of functional connectivity. Here we applied these three approaches to provide a comprehensive characterization of functional connectivity with a seed in the left dPMC that a previous meta-analysis of functional neuroimaging studies has identified as playing a key role in motor learning. Using data from two sources (the Rockland sample, containing resting state data and anatomical scans from 132 participants, and the BrainMap database, which contains peak activation foci from over 10,000 experiments), we conducted independent whole-brain functional connectivity mapping analyses of a dPMC seed. RSFC and MACM revealed similar connectivity maps spanning prefrontal, premotor and parietal regions, while the SC map identified more widespread frontal regions. Analyses indicated a relatively consistent pattern of functional connectivity between RSFC and MACM that was distinct from that identified by SC. Notably, results indicate the seed is functionally connected to areas involved in visuomotor control and

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executive functions, suggesting the dPMC acts as an interface between motor control and cognition.

Keywords

motor learning; functional connectivity; resting state; resting state functional connectivity; meta analytic connectivity modeling; structural covariance

1. Introduction

Converging evidence from single cell recordings, human neuroimaging, and neurostimulation paradigms indicate that the dorsal premotor cortex (dPMC) plays an important part in sensorimotor integration, response selection, and motor learning. Importantly, single-cell recording studies in non-human primates indicate the dPMC has limited ability to directly contribute to movement execution (Boudrias et al., 2010; Dum and Strick, 2005), but the region contains a high proportion of cells that respond to sensory cues, motor cues, or both (Weinrich and Wise, 1982). Thus, it has been suggested that the dPMC integrates sensory and motor information (Roland et al., 1980; Weinrich and Wise, 1982). Converging evidence from neuroimaging, neurostimulation, and neuropsychology indicates that the dorsal premotor cortex (dPMC) has a critical role in response selection (Bestmann et al., 2008; Halsband et al., 1993; O'Shea et al., 2007; Rushworth et al., 2003; Zhang et al., 2011). There is also considerable evidence that the left dPMC in particular plays a dominant role in visuomotor integration processes, while the right dPMC is subservient (Bestmann et al., 2008; Hardwick et al., 2013; Schubotz and von Cramon, 2002a, 2002b). Finally, a recent meta-analysis of human neuroimaging studies has shown the left dorsal premotor cortex (dPMC) is consistently activated across a wide range of motor learning paradigms, regardless of movement execution or the hand being used (Hardwick et al., 2013). As of yet, however, the functional network of brain areas which interact with the left dPMC is relatively unclear. Identifying the regions that functionally interact with the left dPMC in humans would therefore further our understanding of how this key node in the sensorimotor system contributes to response selection and motor learning.

Functional connectivity refers to the temporal coincidence of spatially distant neurophysiological events (Friston, 1994). It is often operationalized as a statistical relationship (usually a correlation) between local neurobiological measures, and can therefore be considered as a broad concept rather than one specific methodology. The advent of multiple connectivity analysis techniques in recent years has led to the possibility to assess different aspects of functional connectivity. Resting state functional connectivity (RSFC) is driven by changes in BOLD activity in the absence of an experimental task (for a review see Biswal, 2012). In seed-based correlation analysis, the timecourse of lower frequencies in the BOLD response extracted from a seed region are then compared with those of all voxels across the rest of the brain, with significant positive correlations implying functional connectivity. RSFC analyses offer the advantage of readily examining whole-brain connectivity without the constraint of a particular task. In comparison, Meta-analytic connectivity modelling (MACM) provides a task based approach to functional connectivity. MACM uses databases of activation peaks from neuroimaging studies to identify consistent

co-activations across experiments (Eickhoff et al., 2010). While experiments are retrieved based on activation within a seed region, significant convergence of coordinates outside the seed reflects above-chance co-activation and hence implies functional connectivity. The large scale of the databases from which MACM analyses are derived provide a great strength to the technique (e.g. the BrainMap database contains >10,000 contrasts with >40,000 subjects). Finally, structural covariance (SC) uses the strength of grey matter volume correlations across the brain as an indicator of past co-activity. The underlying notion is that frequent activation leads to plastic changes in grey matter volume (Draganski et al., 2004), and frequently interacting (co-activating) regions thus co-vary in their grey matter densities (see for example Lerch et al., 2006). Thus, while SC uses a structural brain measure (grey matter volume), it crucially hinges upon functional interaction between brain regions following the principle of Hebbian plasticity (Hebb, 1949). Examining relationships in grey matter volume allows assessment of consistent interaction between brain regions throughout development using a clearly defined measure, the physiological basis of which is clearly understood. In that context, it is important to also consider the different scales of integration (cf. Amunts et al., 2014) represented by these different methods: RSFC is a within-subject measure, MACM integrates across group activation findings, and SC is a cross-subjects measure and cannot be determined on a single-subject basis. As previous studies indicate that functional connectivity is associated with correlated gray-matter volumes (Seeley et al., 2009), we therefore regard it as a ‘functional connectivity’ measure (or, more precisely, a proxy for long-term functional connectivity patterns) for the purposes of this paper. While the degree to which SC can be used to infer functional networks has yet to be established (Clos et al., 2014), it provides a further method for investigating coactivity with the seed region.

Thus, RSFC, MACM, and SC are well established techniques with the common goal of identifying brain networks interacting with the seed region, and may be used to assess ‘functional connectivity’ in the human brain. Each of these techniques probes ‘functional connectivity’ from a different angle, and has specific strengths and limitations. However, combining these tools provides a means to identify the core network of brain areas that consistently interacts with the chosen seed. To date, however, relatively few studies have yet directly compared results from these differing approaches. Recent papers combined the results of RSFC and MACM analyses have suggested good correspondence between the two methodologies (Bzdok et al., 2013; Clos et al., 2014; Hoffstaedter et al., 2013a; Jakobs et al., 2012; Müller et al., 2013; Rottschy et al., 2013). Results from comparisons of RSFC and SC also report correspondence between the two methodological approaches (Segall et al., 2012). While a combination of RSFC, MACM, and SC has previously been implemented as a method for parcellation, (Kelly et al., 2012), only recently has a comparison of seed-based functional connectivity patterns arising from these three techniques been considered (Clos et al., 2014). As all three techniques use different methods to measure the same construct, comparing and contrasting their results provides a more comprehensive overview of ‘functional connectivity’. In particular, a triangulation of their results would provide compelling evidence of the core functional connectivity with the seed region.

The importance of the left dPMC as a hub for sensorimotor integration makes it a prime candidate for examination using functional connectivity techniques. A recent meta-analysis

has identified an area of the left dPMC that was the only region to consistently show increases in activity across a wide variety of motor learning paradigms (Hardwick et al., 2013). This essential role of this region in motor learning has not been recognized in previous models, which have primarily focused on the roles of the primary motor cortex and cerebellum in motor learning (e.g. Krakauer and Mazzoni, 2011). Identifying regions that functionally interact with this seed will therefore further our understanding of the network of areas that may contribute to motor learning. Here we applied RSFC, MACM, and SC connectivity mapping techniques to provide a comprehensive overview of functional connectivity with this left dPMC seed region.

2. Material and Methods

2.1 Seed Region

A seed region in the left dPMC was defined based on the results of a recent meta-analysis of motor learning (Hardwick et al., 2013). This 35mm³ region (peak MNI coordinates -32, -12, 60) survived a series of conjunctions across multiple subanalyses. These subanalyses strictly controlled for potentially confounding activations related to movement execution (i.e. considered only contrasts that compared movement during learning with execution of a similar baseline movement), and controlled for potential laterality effects due to the hand being used to perform the task. This area was therefore consistently activated across a wide variety of motor learning tasks. Data from two sources were utilized to assess functional connectivity with this seed region.

2.2 Data Sources

2.2.1 The Rockland sample—The RSFC and SC analyses used data from the Nathan Kline Institute “Rockland” cohort (Nooner et al., 2012), available online via the International Neuroimaging Data sharing initiative (http://fcon_1000.projects.nitrc.org/indi/pro/nki.html). The sample used from this cohort consisted of 132 healthy subjects (78M, 54F), aged 18-85 years (mean±SD: 42.3 ± 18.1 years). This sample was chosen as it provides a representative sample, and thus provides results that can be assumed to be representative of the general population.

2.2.2 The BrainMap database—The MACM analysis was conducted using the BrainMap database (Laird et al., 2011), using group average peak activation coordinates from neuroimaging studies examining within-subject contrasts in healthy individuals (“normal mapping”, i.e., excluding any interventions such as pharmacological challenges, any longitudinal designs, and patient data, any between-group comparisons to test for differences, e.g., between genders). The BrainMap database was employed to identify task-based co-activation patterns across a large pool of neuroimaging experiments. At the time of processing the database contained stereotaxic peak activation data including approximately 85,000 coordinates (foci) drawn from over 40,000 subjects across more than 10,000 experiments.

2.3 Functional Connectivity Analyses

2.3.1 Seed-based Resting State functional connectivity—Images were acquired using a Siemens Tim Trio 3T scanner using blood-oxygen-level-dependent (BOLD) contrast (260 whole brain echo-planar imaging (EPI) volumes per subject, gradient-echo EPI pulse sequence, repetition time (TR) = 2.5s, echo time (TE) = 30ms, flip angle = 80°, in-plane resolution = $3 \times 3\text{mm}^2$, 38 axial slices (3mm thickness)). A Seed-based RSFC analysis compares endogenous fluctuations of BOLD activity in the seed region with that of all other voxels in the brain as a marker of functional connectivity under task-free conditions. Data were analyzed using SPM8 (Wellcome Trust Centre for Neuroimaging, London). The first four scans were discarded prior to analysis to allow for magnetic field saturation. The images were then corrected for movements by affine registration using a two-pass procedure. In the first step images were aligned to the initial volumes, then subsequently to the mean of all volumes. The mean EPI image for each subject was then spatially normalized to the Montreal Neurological Institute (MNI) single-subject template (Holmes et al., 1998) using the unified segmentation approach (Ashburner and Friston, 2005). The resulting deformation was applied to the individual EPI volumes and images smoothed using a 5-mm full width half maximum (FWHM) Gaussian kernel. Spurious correlations for the time-series of each voxel were reduced by regressing out the nuisance variables of 1) the six motion parameters derived from image realignment; 2) their first derivatives; 3) mean GM, WM and CSF intensity. Nuisance variables were entered into the model as first and second order terms (see Satterthwaite et al., 2013 for an evaluation of this approach). In a final step the data was band-pass filtered with cut-off frequencies of 0.01-0.08Hz. Meaningful resting state correlations occur predominantly within this frequency band due to the low-pass filter like effect of the BOLD signal (Fox and Raichle, 2007; Power et al., 2012).

The time course was extracted from the functionally defined left dPMC seed volume for each subject by computing the first eigenvariate of the time-series' of those voxels whose grey-matter probability was above the median across all voxels in the ROI. Linear (Pearson) correlation coefficients were computed between this seed time-series and the time series of all other grey matter voxels in the brain (Reetz et al., 2012; zu Eulenburg et al., 2012). The voxel-wise correlation coefficients were transformed into Fisher's z-scores and tested for consistency across subjects by a second-level ANOVA (including non-sphericity correction). This random effects analysis was family wise error (FWE) corrected with a cluster level threshold of $p < 0.05$ (cluster forming threshold of $p < 0.001$ at voxel level).

2.3.2 Meta-analytic connectivity modelling—Meta-analytic connectivity modelling (MACM; Eickhoff et al., 2010; Robinson, Laird, Glahn, Lovallo, & Fox, 2010) assesses connectivity by determining brain areas that co-activate above chance with a seed region across multiple neuroimaging experiments. First, all experiments in the BrainMap database with at least one peak activation coordinate within the functionally defined left dPMC seed region were identified. Custom written MATLAB scripts were then utilized to conduct an Activation Likelihood Estimation (ALE) meta-analysis (Eickhoff et al., 2012, 2009; Turkeltaub et al., 2012, 2002) across these in order to identify areas of converging activity across these experiments. The ALE algorithm empirically determines whether spatial convergence of foci between studies is greater than expected by chance. The highest

convergence between studies evidently occurs within the seed (as all included experiments were selected based upon activity within the seed region). Significant convergence in areas beyond the seed is indicative of consistent co-activation (i.e. functional connectivity) with the seed region. Inference in the MACM analysis was conducted at $p < 0.05$ level (corrected for multiple comparisons using permutation testing, controlling cluster-level FWE at $p < 0.05$). While it is possible to restrict the sample of studies that are examined by MACM analyses, for instance, to examine only studies looking at motor control (cf. Hoffstaedter et al., 2013), we here considered all studies within the BrainMap database. A pre-selection would introduce a bias not present in the RSFC and SC analyses. Selecting studies based on the location of their activations alone, however, provides a purely objective and data-driven approach to the MACM analysis. This allowed for unbiased comparisons between the results of the RSFC, MACM, and SC analyses.

2.3.3 Structural Covariance—Structural covariance examines functional connectivity via correlations between regional grey matter properties such as volume or cortical thickness (Albaugh et al., 2013; He et al., 2007b; Lerch et al., 2006). Here we used local volume as estimated by Voxel-Based Morphometry (VBM) on the anatomical T1 weighted MPRAGE scans from the 132 subjects in the Rockland sample to assess structural covariance. Images were acquired using a Siemens Tim Trio 3T scanner as per the Rockland sample protocol (MPRAGE sequence, repetition time (TR) = 2.5s, echo time (TE) 3.5ms, flip angle = 8° , in-plane resolution = $1 \times 1\text{mm}^2$, 192 sagittal slices (1mm thickness). The anatomical scans were preprocessed using the VBM8 toolbox (dbm.neuro.uni-jena.de/vbm) in SPM8 using standard settings (DARTEL normalization, spatially adaptive non-linear means denoising, a Markov random field weighting of 0.15 and bias field modelling with a regularization term of 0.0001 and a 60mm FWHM cutoff). These normalized grey matter segments, modulated only for the non-linear components of the deformations into standard space, were smoothed using an 8mm FWHM Gaussian kernel (this normalization process accounts for differences in grey matter volumes between subjects). Statistical analysis was conducted in FSL1 with non-parametric statistics using the FSL ‘permute’ function (Jenkinson et al., 2012; Smith et al., 2004). The volume for the functionally defined dPMC seed was computed in each subject by integrating the modulated voxel-wise grey matter probabilities under the seed cluster. This subject-specific local volume for the dPMC seed was used as the covariate of interest in the statistical group analysis. Statistical analysis was performed using the standard GLM implementation in FSL testing for each voxel whether the local volume of that particular voxel significantly covaried with the volume of the dPMC. Age was included in the statistical model as a variable of no interest. Inter-individual differences in brain volume were not included in the statistical model, because they were already accounted for in the grey-matter probability maps (grey matter probability maps were modulated by non-linear components, and the analysed voxel values represent the absolute amount of tissue corrected for individual brain size). Significance was assessed at $p < 0.05$ as implemented by FSL (corrected for multiple comparisons using full permutation testing of TFCE images, threshold-free cluster enhancement; Smith & Nichols, 2009).

2.4 Difference Analyses

Difference analyses identified which brain areas were most strongly associated with each functional connectivity mapping technique (Jakobs et al., 2012). These analyses were conducted in a multi-stage process. First, subtraction analyses were generated to compare the results from each functional connectivity analysis. The results of these subtraction analyses were combined in a conjunction on the minimum value, and masked by the original functional connectivity maps. The resulting image was thresholded to provide a map of regions with significantly higher connectivity values than in the counterpart analyses. For example, to generate the map of areas that were more strongly associated with RSFC, the first step was to compute two subtraction analyses (RSFC minus MACM, RSFC minus SC). These difference analyses were combined in a conjunction, which identified the lowest value from each analysis for each voxel. The resulting voxels thus were significantly stronger connected to the seed in RSFC than in either of the two other techniques. Results were then masked by the original RSFC map (ensuring that regions most strongly associated with the RSFC technique would have to demonstrate significant connectivity during the original RSFC analysis). Finally, the resulting map was thresholded such that only voxels with a z-score greater than 1.96 (i.e. $p < 0.05$) were presented. The resulting map indicates which areas are more strongly associated with one of the examined connectivity mapping techniques compared to the other two methods.

2.5 Conjunction Analyses

Conjunction analyses determined areas that were consistently activated across multiple brain connectivity approaches. Pairwise conjunctions were conducted between the three connectivity analyses in order to identify common results across the differing techniques. In addition, a combined analysis was performed across the results of RSFC, SC, and MACM. This combined conjunction thus identified areas with highly consistent functional connectivity to the left dPMC seed region. All conjunctions were computed by taking the minimum statistic (Jakobs et al., 2012; Nichols et al., 2005). Data from MACM were transformed from 2mm^3 MNI space to 1mm^3 for comparison with the RSFC and MACM data.

2.6 Volume Comparisons

Previous studies have suggested that the volumes identified by RSFC, MACM, and SC show 'good convergence' (Bzdok et al., 2013; Clos et al., 2014; Hoffstaedter et al., 2013a; Jakobs et al., 2012; Müller et al., 2013; Rottschy et al., 2013). This has, however, been primarily examined through visual overlay of the identified maps, without further quantification. Here we compared the volumes identified by each analysis, then quantified the volumes that were either uniquely identified by one analysis, or were identified by multiple analyses via conjunction.

2.7 Volume-Matched Analyses

Differences in the approaches employed by each of the analyses led to differences in the size of the total volumes of the brain that were identified as having functional connectivity with the motor learning-related seed region. A control analysis therefore aimed to determine

whether the different functional connectivity mapping techniques examined identified broadly similar patterns of connectivity that differed mainly due to differences in statistical thresholding, or whether the different techniques identified truly divergent networks. The network with the smallest overall volume was identified (the MACM map, with a volume of 76,749mm³). The thresholds of the RSFC and SC connectivity maps were then iteratively increased until the volumes they identified were approximately equal to that of the MACM network. Further volume comparison analyses were then conducted on the volume-matched maps.

2.8 Labelling

Results were anatomically labelled according to their most probable macroanatomical and cytoarchitectonic locations using the SPM Anatomy Toolbox (Eickhoff et al., 2007, 2005). Additional labels were derived from a functional meta-analysis of motor cortical regions (Mayka et al., 2006). Peak maxima of the reported coordinates are presented in 1mm³ MNI space. Only regions with 100 cohesive voxels were reported.

3. Results

3.1 Main analyses

3.1.1 Resting state Functional Connectivity—The RSFC analysis (Figure 2A) identified regions where the BOLD timecourse correlated with that in the left dPMC seed volume. This analysis revealed a distributed network that contains large clusters in frontal and parietal regions, and smaller clusters in occipitotemporal cortex, striatum and cerebellum. Connectivity with most regions was bilaterally, but stronger in left supratentorial regions and right cerebellar regions, consistent with its connectivity with left-lateralized seed. Specifically, a widespread frontal cluster spanned premotor regions including the pre-SMA and SMA, ventral and dorsal premotor cortex, and extended into bilateral dorsolateral prefrontal cortex, left IFG and the left anterior insula. A second large bilateral parietal cluster spanned left inferior and superior parietal lobules, and the bilateral precuneus. In addition, connectivity was found with the mid-cingulate gyrus, bilateral fusiform gyrus, and bilateral ventral occipitotemporal cortex roughly corresponding with area V5. This analysis was the only one to identify striatal and cerebellar regions. Specifically, RSFC connectivity was found with bilateral thalamus, bilateral dorsal striatum. Cerebellar connectivity was more pronounced in the right cerebellar hemisphere, with a large cluster spanning lobules HVI and HVII (Crus I and II), and a smaller cluster in lobule HVIII. In the left cerebellar hemisphere, smaller clusters were present in lobules HVII (Crus I and II) and HVIII.

3.1.2 Meta-analytical connectivity mapping—MACM (Figure 2B) provided the most restricted network of all three connectivity mapping techniques examined, revealing a bilateral network of fairly localized premotor and posterior parietal cortical structures (see Table 2). Consistent task based co-activation with the left dPMC seed region was identified in the contralateral dPMC, and bilateral vPMC, SMA and IFG, extending into the anterior insula. Additional connectivity was found in localized clusters in the left ventral occipitotemporal cortex, bilateral precuneus and intraparietal cortex, along with smaller

clusters in the right angular gyrus and superior parietal lobule. The MACM analysis was unique in identifying connectivity with the left anterior insula. The MACM analysis did not reveal connectivity with subcortical regions.

3.1.3 Structural covariance—The SC analysis (figure 2C) revealed areas where the grey matter volume correlates with the grey matter volume in the left dPMC seed region. This analysis yielded large areas spanning most of the frontal lobe, from the primary motor cortex to the orbitofrontal cortex. Smaller clusters were identified in the temporal and parietal lobes (see Table 3). The pattern was largely bilateral but stronger on the left, consistent with a left-lateralized seed. Frontal significant grey matter correlations were found bilaterally with the dPMC, IFG, SMA, and primary sensory and motor cortex. Unique to the SC analysis, connectivity was also identified with mid-cingulate cortex, left middle temporal gyrus, right temporal pole, bilateral cuneus and occipital gyrus. Notably, no clusters were identified in the parietal cortex, or in any subcortical regions.

3.2 Difference Analyses

3.2.1 Resting State Functional Connectivity > (Meta-Analytic Connectivity Modelling & Structural Covariance)—Consistent with the very robust pattern of activation revealed by the RSFC analysis, the pattern of regions more strongly associated with this analysis (Figure 3A) is very similar to that identified in the main analysis (Figure 2A). The clusters most strongly associated with RSFC spanned bilateral premotor and supplementary motor regions stretching into dorsolateral prefrontal cortex and anterior insula, as well as large areas of bilateral precuneus, superior and inferior parietal lobules, fusiform gyrus and ventral occipitotemporal cortex. As the cluster in the left thalamus, bilateral putamen and bilateral cerebellar regions were only identified as having connectivity with the seed by the RSFC analysis, the same pattern of subcortical activity were evidently more strongly associated with RSFC than the other techniques examined. Thus, most regions identified by the RSFC analysis, were more strongly identified with this method than with the either structural covariance modelling or meta-analytic connectivity modelling.

3.2.2 Meta-Analytic Connectivity Modelling > (Resting State Functional Connectivity & Structural Covariance)—Areas in which MACM was stronger than RSFC and SC were relatively small in volume. These areas included the bilateral anterior insula, left dPMC (slightly dorsal from the seed region) and right vPMC, as well as small clusters in the left inferior occipital gyrus and the superior parietal lobule (see Figure 3B). Of these regions, the right ventral prefrontal cortex and right anterior cingulate cortex were solely identified in the MACM analysis. In the parietal and occipital brain areas, RSFC and MACM overlapped substantially, but small clusters were more strongly present in the MACM.

3.2.3 Structural Covariance > (Resting State Functional Connectivity & Meta-Analytic Connectivity modelling)—Structural covariance yielded the strongest connectivity measures bilaterally across large areas of the frontal lobe and medial wall (see Figure 3C). In the majority of these areas, the correlation of the grey matter volume between the dPMC seed with the grey matter volume in these regions, while the other two methods

did not reveal significant connectivity with dPMC. Particularly striking are the robust bilateral clusters in the primary motor cortex, as well as the spread of the prefrontal cluster which extended into bilateral orbitofrontal gyrus and right frontal and temporal pole (see Figure 3B). In addition, smaller clusters were found in the left superior temporal gyrus, left precuneus and bilateral cuneus.

3.3 Conjunction Analyses

Several conjunction analyses were carried out to shed light on regions commonly identified by the different connectivity analyses. The areas commonly identified in the RSFC and MACM analyses were fairly localized bilateral clusters in frontal and parietal lobes, with larger clusters ipsilateral to the left dPMC seed region (see Figure 4A). These clusters were present in the right dorsal and ventral premotor cortex, supplementary motor cortex, and the left ventral premotor cortex extending into dorsolateral prefrontal cortex and inferior frontal gyrus. Bilateral parietal clusters were present in the intraparietal sulcus and superior parietal lobule. The conjunction of analyses based on the Rockland sample (i.e. RSFC and SC analyses) revealed a widespread network spanning bilateral prefrontal and motor cortex, along with a few much smaller clusters in the superior parietal lobule and precuneus (see Figure 4B). Only a small number of regions were commonly identified by SC and MACM analyses; these were in left vPMC, SMA and right dPMC. (see Figure 4C). Finally, the combined conjunction of all three connectivity analyses (i.e. RSFC, MACM, and SC; see Figure 4D) was very similar to the conjunction of the MACM and SC analyses. Specifically, these areas were left vPMC, right dPMC, and the SMA.

3.4 Volume Quantification

We quantified the volumes identified in each analysis to further investigate the differences and similarities between RSFC, MACM, and SC. We first quantified the total volumes identified by the RSFC, MACM, and SC analyses (Figure 5A). RSFC identified the largest overall volume with functional connectivity with the seed ($381,166\text{mm}^3$). The RSFC network was more than double the size of the SC network ($179,839\text{mm}^3$), while the SC network was in turn more than double the size of the MACM network ($76,749\text{mm}^3$).

We then compared the convergence and divergence of the networks as examined in the conjunction analyses. Overlaying the RSFC and MACM networks (Figure 5B) revealed that 81% was unique to the RSFC analysis, while only 3% was unique to the MACM analysis. The remaining 16% of the overall volume was identified as surviving the conjunction of RSFC and MACM. Due to the disparity of their sizes, this meant that the majority of the volume identified in the MACM analysis was also identified by the RSFC analysis (see Venn diagram illustrating overlap, Figure 5B). Pairwise comparisons indicated that 17% of the volume identified by RSFC analysis survived conjunction with the MACM map (see Figure 5F), while 83% of the MACM map survived conjunction with the RSFC map (see Figure 5G). Overlaying the RSFC and SC networks (Figure 5C) revealed that 64% of the total volume identified was unique to RSFC, while 24% was unique to SC. Thus, 12% of the total volume identified in both analyses was shown to be commonly found in both techniques. Pairwise comparisons of these maps revealed that 16% of the RSFC map survived conjunction with the SC map (see Figure 5H), while 34% of the SC map survived

conjunction with the RSFC map (see Figure 5I). Overlaying the MACM and SC networks (Figure 5D) showed that 67% of the total network was unique to the SC analysis, while 23% was unique to the MACM analysis, and 10% was commonly identified in both maps. Pairwise comparisons showed that 29% of the MACM map survived conjunction with the SC map (see Figure 5J), while 12% of the SC map survived conjunction with the MACM map 2(see Figure 5K).

Finally, we considered the divergence and convergence between the RSFC, MACM and SC maps in a combined analysis, overlaying all three functional connectivity maps. The majority of the volume identified by all three mapping techniques was unique to RSFC (54%) or the SC analysis (23%). A relatively small volume was identified only by MACM (2%). Conjunctions indicated similar overall volumes were identified by both RSFC and MACM but not SC (8%), or RSFC and SC but not MACM (9%). In comparison, the volume identified by both MACM and SC but not RSFC was extremely small (1%). Considered relative to the total volume identified by all three analyses, only a small volume was identified in the combined conjunction of the RSFC, MACM, and SC analyses (4%).

3.5 Volume-Matched Analyses

Results of the volume matched control analysis were similar to those of the main analyses: RS and MACM identified relatively consistent networks of frontal, premotor and parietal regions. In comparison, SC revealed a network of areas more local to the seed, consisting mainly of prefrontal and premotor regions.

3.6 Volume-Matched Analyses: Volume Comparisons

Volume-matched analyses controlled for potential differences in the maps identified by each network arising from differences in the sizes of the volumes they identified. The volume-matched analysis iteratively increased the threshold of the RS and SC maps, reducing their volumes until they were approximately equal to that of the MACM analysis (See Figure 7A). Overlaying the maps identified by the RSFC and MACM analyses showed that 24% of this volume was common to both analyses. 39% of the volume of the volume-matched RSFC map survived conjunction with the MACM map, and (due to the volume matching approach), 39% of the MACM map survived conjunction with the RSFC map (see Figure 7F-G). Overlaying the volume-matched RSFC analysis with the volume-matched SC analysis identified an 8% overlap (Figure 7C). Of the volume-matched RSFC map, 15% survived conjunction with the volume-matched SC map, and vice versa (figure 7H-I). Overlaying the MACM map on the volume-matched SC map identified that 10% of the maps overlapped (Figure 7D). For the MACM map, 18% survived conjunction with the volume-matched SC map, and vice versa (Figure 7J-K). A combined overlay analysis of all three maps also identified that the volume-matched SC analysis had the least overlap with other networks, consistent with the main analysis (Figure 7E).

4. Discussion

The dPMC plays an essential role in integrating sensory and motor information (Roland et al., 1980; Weinrich and Wise, 1982), and the left dPMC in particular is consistently

activated during a wide range of motor learning tasks (Hardwick et al., 2013). Despite the importance of the dPMC for sensorimotor integration and motor learning, there is limited understanding of the areas that functionally interact with it. The present study therefore examined regions that have functional connectivity with a left dPMC region key to motor learning (Hardwick et al., 2013). We employed resting state functional connectivity, (RSFC), Meta-Analytic Connectivity Mapping (MACM), and Structural Covariance (SC), comparing and combining their results to provide a comprehensive overview of connectivity with the seed. The maps resulting from the RSFC, MACM, and SC analyses identified networks of varying size and topography. Notably, the maps from the RSFC and MACM analyses were qualitatively similar, primarily spanning premotor and parietal regions. In comparison, the SC map identified predominantly frontal and temporal regions.

The differences between the maps for RSFC, MACM, and SC may be attributed to the methodological approaches employed by the three techniques. RSFC networks are based on “spontaneous”, task-free fluctuations in the BOLD signal, while MACM is based upon convergence of peak co-activity between task based fMRI and PET experiments. Thus, the signals from RSFC and MACM are similar in that they both primarily encapsulate short term blood utilization in brain tissue. Note, however, that the RSFC analysis used only data from fMRI, while the MACM analysis amalgamated data from both fMRI and PET; these different modalities are known to influence activation profiles (Veltman et al., 2000), which could contribute to the differences seen between the RSFC and MACM analyses. In comparison, SC identifies correlations in grey matter volume between brain regions, and as such has less in common with RSFC and MACM. In addition, RSFC and MACM relate to comparatively short time spans, considering functional connectivity at rest (RSFC) or during the performance of specific tasks (MACM). The time span for SC is much longer, assessing differences in grey matter volume that have arisen throughout life thus far. An additional consideration is that the present study aimed to gain a comprehensive overview of functional connectivity with the dPMC seed region by examining *typical* applications of RSFC, MACM and SC. As such there are methodological differences between implementations, as is the case when each technique is used individually in the present literature. While it could be argued that standardizing these approaches may have reduced between-technique noise, such an approach would lead to questionable methodological choices; for instance, it is not feasible to assess VBM data (as used in SC) using cluster-level inference, which is standard in RSFC and MACM. Furthermore, attempting to rigidly match these procedures may artificially promote homogeneity of the results. The present approach therefore allows further generalization of the results, allowing comparison of each individual analysis with those presently found in the literature.

A further consideration is that none of these techniques can perfectly capture functional connectivity, as each are subject to different sources of inherent noise. The spontaneous BOLD signal from which RSFC is derived is thought to be particularly susceptible to artefacts from preprocessing and physiological noise (Chang and Glover, 2009; Power et al., 2012). MACM is derived from peak coordinates from task-based fMRI and PET studies, and is thus constrained by the tasks possible to be performed in the scanner and the inherent spatial uncertainty of neuroimaging results (Eickhoff et al., 2009; Rottschy et al., 2012).

Finally, as well as representing experiences such as repeated practice of motor tasks (e.g. Gaser and Schlaug, 2003), differences in brain structure detected by SC are influenced by both environmental and hereditary factors throughout development (Alexander-Bloch et al., 2013).

To date, relatively few studies have compared results from all three of these techniques; most have compared RSFC with either MACM or SC (Bzdok et al., 2013; Jakobs et al., 2012; Rottschy et al., 2013; Segall et al., 2012). These investigations have generally reported that the two techniques they have examined provide qualitatively similar results. Here we extended this work by quantifying the volumes identified by each analysis and their conjunctions, which further illustrated the relative similarities between the RSFC and MACM networks in comparison to the results of the SC analysis. Notably, RSFC and MACM are well established methods for mapping functional connectivity (Biswal, 2012; Robinson et al., 2010), while the degree to which anatomical covariance networks as identified by SC are representative of functional connectivity is debatable (Clos et al., 2014). As a result we first discuss the common functional connectivity network as identified by RSFC and MACM, then consider the added benefit and potential problems to consider when comparing their results to SC.

4.1 Areas with consistent functional connectivity: Networks for Motor Learning Identified by RSFC and MACM

As noted above, visualization of connectivity maps and volume quantifications indicated considerable convergence between the RSFC and MACM maps. Conjunction of these maps identified a consistent network of brain regions with functional connectivity to the motor learning related seedregion, including the right dPMC, bilateral ventral premotor cortex (vPMC), bilateral supplementary motor area (SMA), left dorsolateral prefrontal cortex (DLPFC), bilateral posterior parietal cortex, and left a V5/MT. This network is consistent with the role of the left dPMC as a central hub for sensorimotor integration and motor learning.

Interhemispheric dPMC interactions are well documented in motor control. Simple unilateral movements are typically associated with increases in bilateral dPMC activity in both non-human primates (Cisek et al., 2003; Tanji et al., 1988) and humans (Ward and Frackowiak, 2003). The left dPMC is dominant in action selection (Bestmann et al., 2008), though the right dPMC can assume this role if the left dPMC is compromised (O'Shea et al., 2007). Studies of sequence learning have also identified increased right dPMC activity for the perceptual elements of sequences (Schubotz and von Cramon, 2002a, 2002b). The dPMC therefore appears to play a key role in volitional movement preparation, with the left dPMC being dominant for action selection and initiation, and the right dPMC playing a supportive role in acquisition and retrieval. Bihemispheric recruitment of the vPMC is also frequently observed in motor control (Binkofski et al., 1999; Davare et al., 2006; Ehrsson et al., 2001, 2000). The vPMC is specifically involved in the sensory guidance of hand movement (Binkofski et al., 1999), especially in hand shaping for precision grasp (Davare et al., 2006).

The SMA and left dPMC were also not only identified as having consistent connectivity across the RSFC, MACM, and SC analyses here, but were also consistently linked with activation during motor learning in our previous meta-analysis (Hardwick et al., 2013). Moreover, consecutive days of motor training lead to parallel increases in their grey matter volumes (Hamzei et al., 2012). As both are active in motor learning tasks that control for simple motor activity (Hardwick et al., 2013), they therefore appear to play a role in motor learning beyond movement execution itself. Both have been linked with movement sequences; the SMA being more closely associated with those that have been learned extensively (Wymbs and Grafton, 2013). The SMA has also classically been linked with the self-initiation of voluntary movements (Deecke and Kornhuber, 1978; Hoffstaedter et al., 2013b) and in switching between ongoing movement tasks (Nachev et al., 2008; Obeso et al., 2013). Increases in pre-SMA activity have frequently been associated with successful response inhibition (see Obeso et al., 2013; but also Criaud & Boulinguez, 2013). The SMA therefore likely interacts with the dPMC in order to store movement sequences, and to initiate, modify and possibly inhibit (or coordinate the inhibition of) actions.

Lesion studies in non-human primates indicate the DLPFC plays an important role in rule driven action selection (Wise and Murray, 2000). Similarly in humans, the DLPFC is associated with a role for rule representation within the working memory network (Nee et al., 2013). The DLPFC may therefore contribute to motor learning through providing declarative knowledge to be applied to motor output. Interestingly, interfering with the normal function of the DLPFC through theta-burst stimulation or cathodal transcranial direct current stimulation reduces declarative knowledge, but improves motor performance, presumably through placing an increased emphasis on implicit aspects of performance (Galea et al., 2010; Zhu et al., 2015). The DLPFC could therefore interact with the dPMC by providing declarative knowledge and relevant rules to guide motor output (see Wise and Murray, 2000).

The posterior parietal cortex receives multisensory inputs (see Grefkes and Fink, 2005), and is involved in weighting their evidence in order to produce appropriate motor output (Block et al., 2013). Notably, the regions demonstrating parietal connectivity in the conjunction of the RSFC and MACM maps included the superior parietal lobule (SPL), which was also found to be commonly activated in our recent meta-analysis of 70 motor learning experiments (Hardwick et al., 2013; see supplementary methods for comparison). The SPL has known physiological connectivity with the primate dPMC (Matelli et al., 1998), and their interaction is important for visuomotor control (Wise et al., 1997). Thus, multisensory input from the parietal lobe is thought to be processed to become motor output via an SPL-dPMC pathway (Cieslik et al., 2011; Johnson et al., 1996, 1993).

The inferior temporal cortex (ITC) is considered to be part of the ventral visual stream (Gross, 2008). ITC neurons respond only to visual stimuli (Gross et al., 1972, 1967), and are specialized for recognition of shapes regardless of size, color, contrast, or location within the visual field (Schwartz et al., 1983; Rolls and Baylis, 1986). In humans, lesions of ITC lead to visual agnosia, characterized by an inability to recognize visual stimuli (Bauer, 2006). Association of a ventral stream area with motor control may seem surprising, as the dorsal visual stream is classically associated with movement (Goodale and Milner, 1992).

However, functional connectivity with a region specialized in shape recognition is consistent with the essential role of the dPMC plays in producing motor responses to arbitrary visual stimuli (Wise and Murray, 2000).

Notable for a network involving motor control, the primary motor cortex (M1) was not identified as being functionally connected with the seed in the combined RSFC and MACM conjunction. M1 was also absent in the liberal analysis that removed thresholding from the MACM network (see supplementary results). This may seem surprising as there are known physiological connections between dPMC and M1 shown (Dum and Strick, 2005) and as dPMC excitability can affect M1 excitability in humans (Davare et al., 2009). However, RSFC connectivity does not always map onto anatomical connections (Di Martino et al., 2008; Kelly et al., 2010; Uddin et al., 2008; Vincent et al., 2007), and a previous study based on 1,000 subjects that parcellated the brain into RSFC networks did not show functional connectivity between M1 and premotor regions such as dPMC (Yeo et al., 2011). In addition, the absence of M1 from the MACM analysis may in large part be explained by the contrasts present in the Brainmap database. Most neuroimaging studies include controls for simple motor execution (see for examples (Daselaar et al., 2003; Inoue et al., 2000). Importantly, our previous finding that such contrasts remove M1 activation but still show dPMC activation (Hardwick et al., 2013) highlight the importance of the dPMC in higher-order motor processing.

Connectivity with the cerebellum was present in the RSFC analysis. In the right cerebellum, connectivity included regions associated with the lower hand representation in lobule HVIII (Thickbroom et al., 2003; Yeo et al., 2011), consistent with the importance of the cerebellum in motor control (Hardwick et al., 2014, 2013). Bilateral connectivity was also identified with lobules HVII (Crus I and II), which are involved in cognitive and linguistic processes (Lesage et al., 2012; Stoodley and Schmahmann, 2009), and are functionally connected to DLPFC and PPC (Buckner et al., 2011; O'Reilly et al., 2010). Given the importance of the cerebellum in motor control and learning, and the presence of cerebellar clusters of connectivity with the dPMC in the RSFC analysis, the absence of cerebellar clusters in the MACM analysis is perhaps surprising (though the MACM analysis did not identify the cerebellum as having functional connectivity with the dPMC, further analysis did identify multiple subthreshold clusters of cerebellar connectivity - see supplementary results). This difference can likely be attributed to the focus that many functional imaging studies place on imaging the cerebral cortex; the standard normalization process conducted in neuroimaging studies is not optimized for the cerebellum (Diedrichsen, 2006). Furthermore, inferior portions of the cerebellum are sometimes not covered by the field of view in many whole-brain fMRI studies, and when these regions are acquired the default bounding box for normalization in certain software analysis packages do not include the entire cerebellum. This would lead to the absence of and greater variability in cerebellar coordinates than those in the cerebral cortex for many of the studies included in the BrainMap database, and may explain why the MACM analysis detected clusters in the cerebellum that did not survive thresholding.

4.2 Functional connectivity and Structural covariance

As considered above, RSFC and MACM are previously established methods for identifying functional connectivity with a seed region, while the degree to which SC can determine functional connectivity is currently a subject of ongoing debate (Clos et al., 2014). Notably, while RSFC and MACM identified a similar network of frontal, premotor and parietal regions, SC identified a network of mainly frontal regions that was more widespread than that revealed by the other two methods. This is consistent with findings from graph-theoretical SC analyses that report predominantly local connectivity (He et al., 2007a), and with data from seed-based SC analyses that identify regions largely limited to the lobe in which of the seed is defined (Clos et al., 2014; Seeley et al., 2009; Zielinski et al., 2010). SC is thought to represent a combination of developmental coordination or synchronized maturation between brain areas (Alexander-Bloch et al., 2013). The SC network identified here is consistent with both of these properties; the prefrontal, premotor, and motor regions identified by SC are highly interconnected via anatomical fiber tracts (Bürgel et al., 2006, 1999; Carmichael and Price, 1995; Dum and Strick, 2005), and develop concurrently (Giedd et al., 1999).

4.3 The Rockland Sample and the BrainMap Database

The RSFC and SC analyses in the present study used whole brain neuroimaging data from the Rockland sample. As data from the same subjects were used in both the RSFC and SC analyses, these analyses are therefore matched for factors such as age and gender. In contrast, the MACM analysis was based on data from the BrainMap database, which reports stereotaxic peak activation coordinates from published neuroimaging studies. Using peak coordinates leads to the loss of spatial information, but provides a pragmatic solution to the problems associated with sharing large datasets (current technical and practical limitations prevent the storage of whole brain data from the 10,000+ neuroimaging studies included in the BrainMap database). Moreover, in spite of beginning data-sharing efforts, integrating published maxima coordinates are currently the only approach that allows summarization of the entire current literature. This loss of spatial information may account for the relatively small size of the volume identified by the MACM analysis in comparison to the RSFC and SC analyses. However, while these coordinates present a relatively sparse representation of the original activation maps they encapsulate, they also represent the most probable locations of activity from the activation maps they encapsulate, and thus provide a highly reliable source of data. Differences in sampling demographics may also influence the connectivity maps identified by each technique. The Rockland sample aims to produce a representative sample of individual subjects from the general population; in contrast, the BrainMap database stores average information from groups of subjects, and the papers from which this information is drawn to not always report demographic information in a uniform manner (e.g. some papers report mean subject ages, some report only age ranges, etc). Similarly, it may be expected that the corpus of studies and contrast types contained within the BrainMap database could influence the results it provides; for example, as most studies require participants to visual stimuli (vs other modalities), there may be a bias toward finding activity in visual regions. However, sample bias effects appear unlikely given the high level of consistency between the MACM and RSFC maps (the latter of which by definition is not affected by task demands). Furthermore, it is notable that this study and

others have identified similar results using RSFC and MACM (Bzdok et al., 2013; Clos et al., 2014; Hoffstaedter et al., 2013a; Jakobs et al., 2012; Müller et al., 2013; Rottschy et al., 2013). The consistency between results from RSFC and MACM illustrate that harnessing the large and varied sample from the BrainMap database can provide a powerful approach to functional connectivity.

5. Conclusions

Here we employed multiple connectivity modelling techniques to identify areas functionally interacting with a left dPMC region identified as key for motor learning. RSFC, MACM, and SC offer different methodological and conceptual approaches to identifying functional connectivity with a seed region, and were used here to provide a comprehensive assessment of functional connectivity with the dPMC (cf. Clos et al., 2014; Reid et al., 2015). Each approach identified networks with clear differences in both their size and topography. However, further analyses indicated that RSFC and MACM revealed a relatively consistent network of prefrontal, premotor, and parietal regions, while the SC map consisted mainly of widespread frontal regions. All techniques identified a consistent ‘core’ network of functional connectivity with the left vPMC, right dPMC, and the SMA, all of which play important roles in the motor control and learning (Hardwick et al., 2013). Most notably, conjunction of the RSFC and MACM networks identified a consistent functional network consisting of the bilateral dPMC, vPMC, SMA, and PPC, as well as left hemisphere connectivity with the DLPFC and ITC. This network is consistent with the established role of the dPMC in response selection, suggesting it supports motor learning by acting as an interface between higher cognitive functions and visuomotor control.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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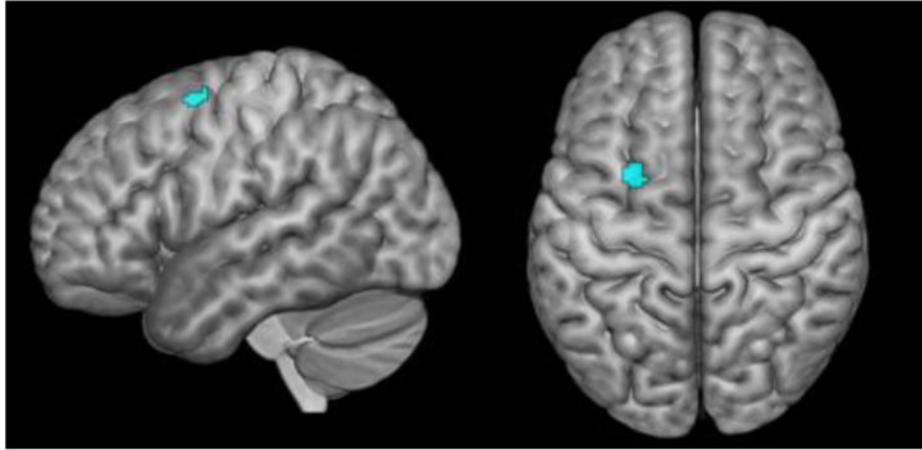


Figure 1.

The left dPMC seed region. A previous meta-analysis of motor learning (Hardwick et al., 2013) identified this seed as a key area for motor learning. The seed region was the sole area surviving multiple analyses that strictly controlled for both movement execution and hand use.

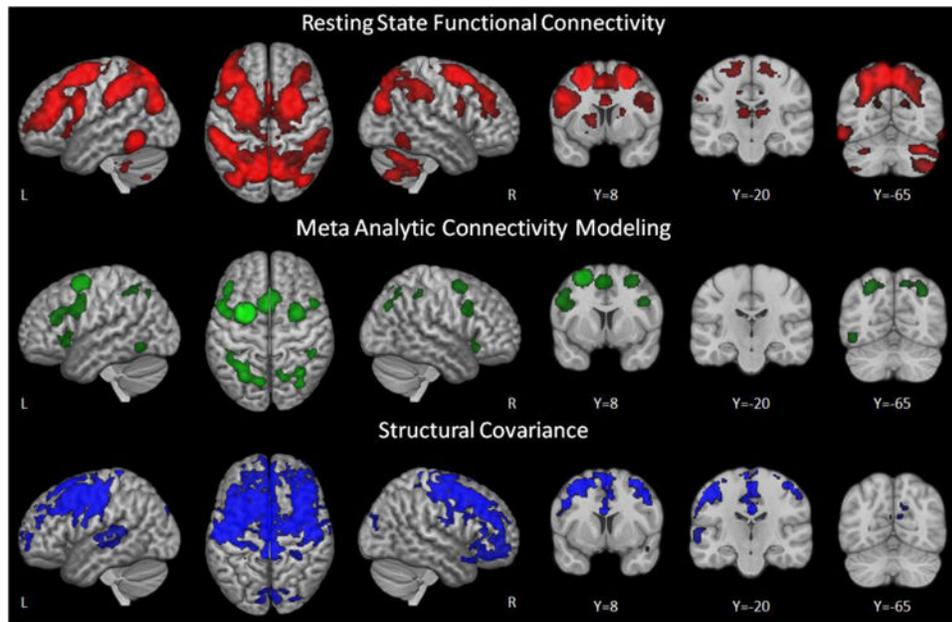


Figure 2. Results of the connectivity analyses. 2A) The resting state analysis (red) revealed the largest functional connectivity network, including frontal-premotor, and parietal cortex, as well as the thalamus, putamen, and cerebellar regions. 2B) Meta-analytical connectivity modelling (green) gave relatively focal results with a bilateral network of premotor and parietal cortical structures. 2C) The structural covariance analysis (blue) identified a large functional connectivity network, with widespread clusters, predominantly in prefrontal and motor/premotor areas.

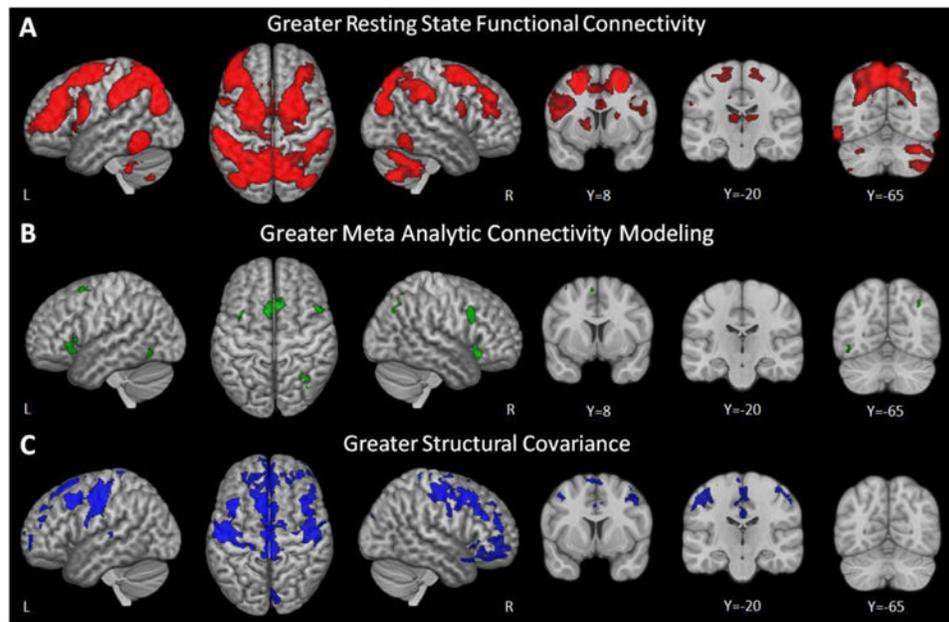


Figure 3. Difference analyses presenting regions where one of the connectivity analyses provided significantly stronger scores than its counterparts. 3A) Results more strongly associated with RSFC, shown with red clusters. 3B) Results more strongly associated with MACM, shown with green clusters. 3C) Results more strongly associated with SC, shown with blue clusters.

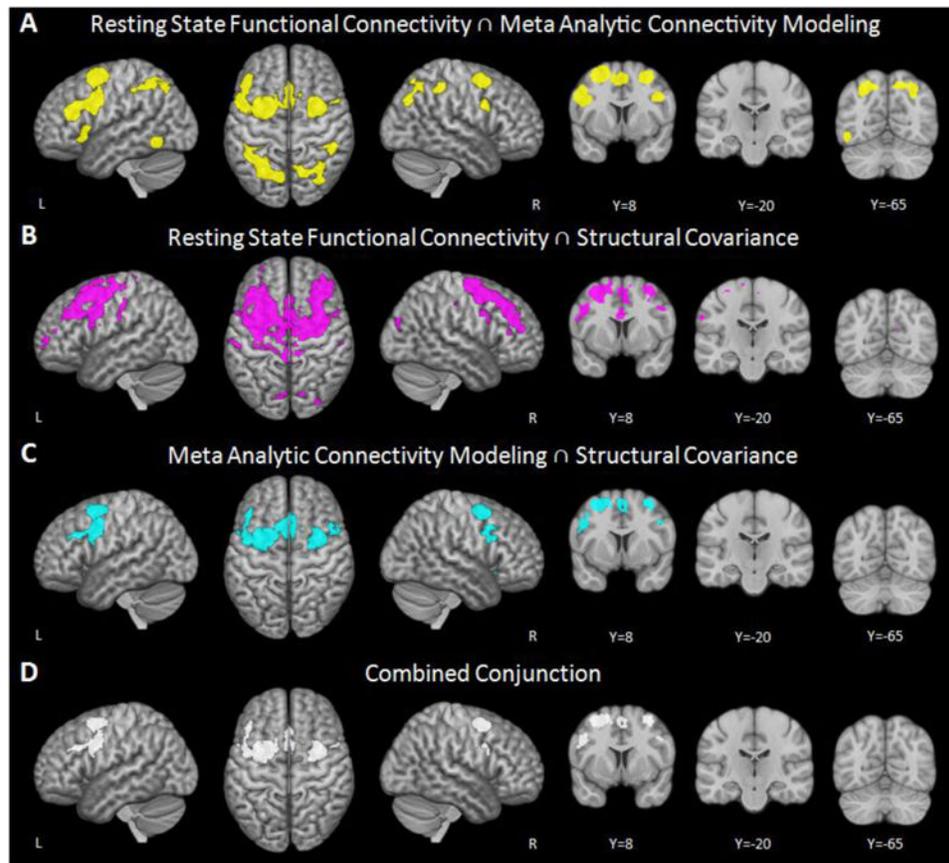


Figure 4. Results of the conjunction analyses. A) Conjunction of the RSFC and MACM analyses. B) Conjunction of the RSFC and SC analyses. C) Conjunction of the MACM and SC analyses. D) A combined conjunction from all three analyses (RSFC, MACM, and SC), identifying a consistent ‘core’ network common to all connectivity mapping techniques considered.

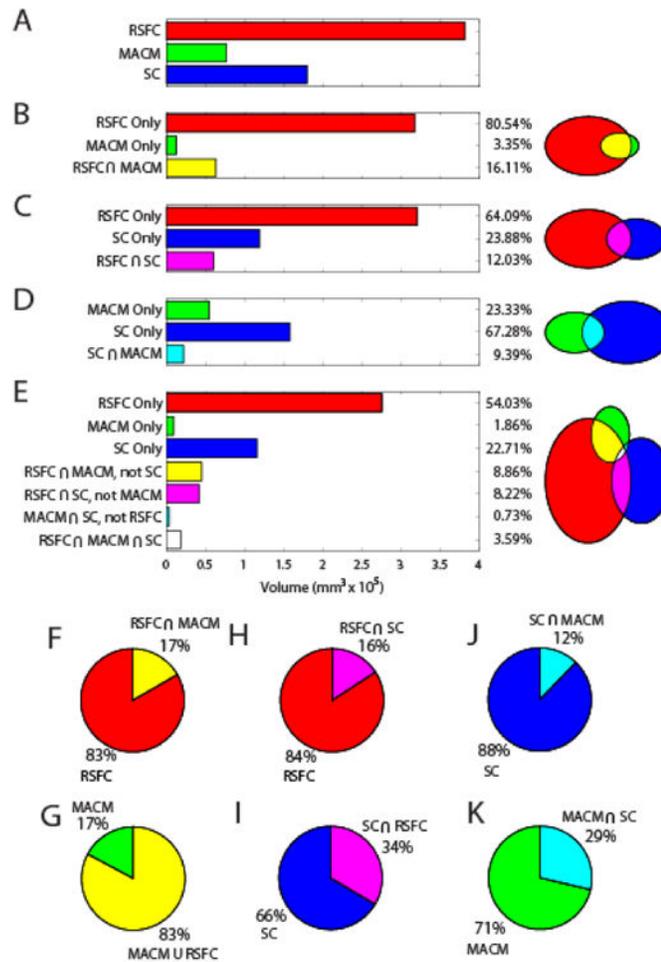


Figure 5. Volume comparisons of the total volumes identified by the analyses, and their unique contributions and overlap. A) Total volumes identified by the RSFC, MACM and SC analyses. Further sections of the figure illustrate the overlap and disparity between total volumes identified by B) the RSFC and MACM analyses, C) the RSFC and SC analyses, D) the SC and MACM analyses, E) The RSFC, MACM, and SC analyses. F-K) pairwise comparisons illustrating the degree of overlap for each combination of analyses.

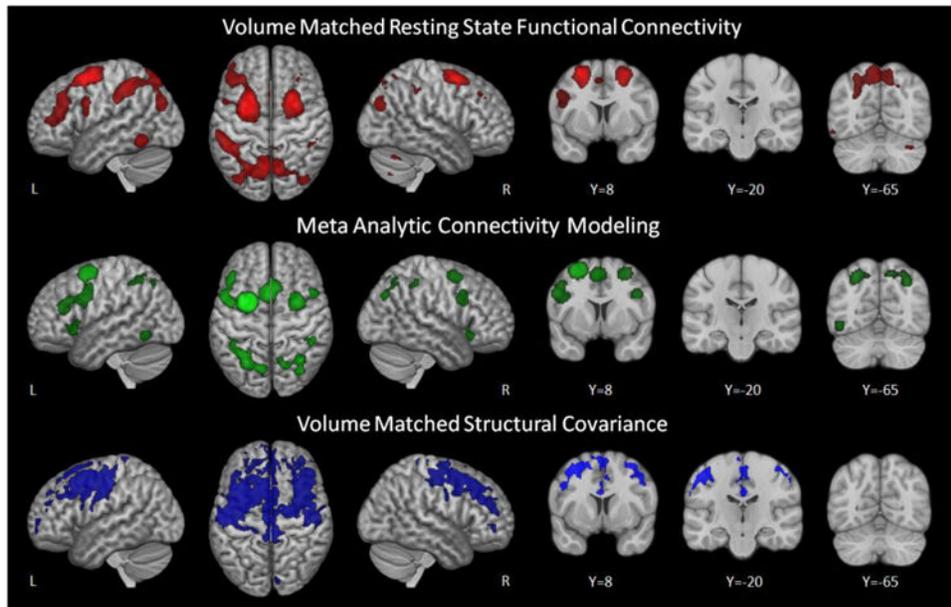


Figure 6. Results of the conservatively thresholded RS and SC analyses in comparison to the results of the MACM analysis

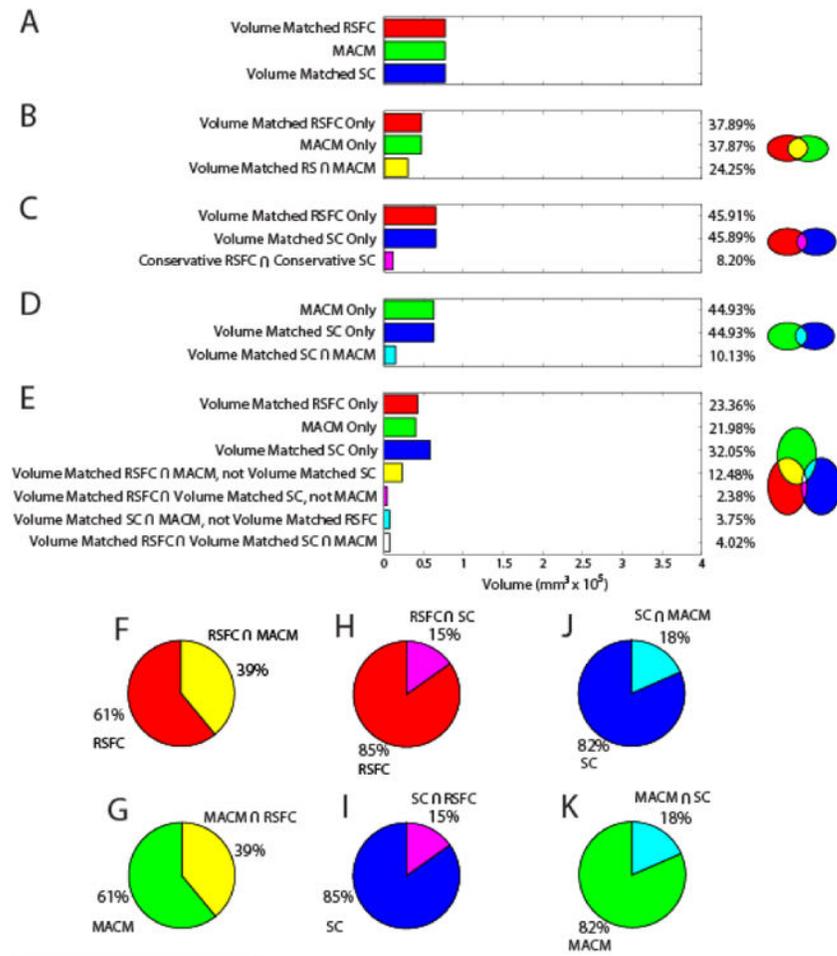


Figure 7. Volume comparisons for the volume-matched analyses

Table 1

Resting state functional connectivity

#	Vol (mm ³)	Macro	Cyto	t-score	MINI Coordinates		
					X	Y	Z
1	172,308	L dPMC		56.21	-26	4	60
			R dPMC	27.62	26	8	56
			L SMA	14.91	-4	22	42
			L vPMC	12.82	-46	6	30
			L Inferior Frontal Gyrus (p. Triangularis)	12.54	-48	36	18
			L Putamen	7.45	-16	8	4
			L Thalamus	7.37	-6	-14	12
			R Thalamus	7.15	8	-20	12
			R vPMC	5.96	50	6	26
			L Precuneus	18.68	-6	-64	54
2	151,208	L Inferior Parietal Lobule	hip2	16.92	-52	-42	48
			SPL (7P)	16.50	-8	-72	54
			SPL (7P)	16.29	8	-70	52
			IPC (PF)	15.53	-52	-34	44
			hip2	15.46	-38	-48	50
			hip1	15.25	-36	-48	48
			SPL (7P)	14.74	-16	-74	54
			Lobule VIIa Crus I (Hem)	12.31	36	-64	-32
			Lobule VI (Hem)	11.71	30	-62	-32
			Lobule VIIa Crus II (Hem)	8.78	38	-68	-52
3	24,072	R Cerebellum	Lobule VIIb (Hem)	8.69	30	-70	-50
			Lobule VIIIb (Hem)	14.95	-58	-58	-14
			Lobule IX (Hem)	7.58	64	-58	-12
			Lobule VIIIb (Hem)	9.67	14	-52	-48
			Lobule VIIIb (Hem)	4.60	12	-62	-62
			Lobule VIIa Crus I (Hem)	7.51	-32	-62	-34
			Lobule VIIa Crus II (Hem)	3.24	-48	-48	-50
			Lobule VIIa Crus I (Hem)	3.24	-48	-48	-50
			Lobule VIIa Crus II (Hem)	3.24	-48	-48	-50
			Lobule VIIa Crus II (Hem)	3.24	-48	-48	-50
4	12,071	L Inferior Temporal Gyrus					
5	4,405	R Inferior Temporal Gyrus					
6	4,205	R Cerebellum					
7	4,063	L Cerebellum					

#	Vol (mm ³)	Macro	Cyto	t-score	MNI Coordinates		
					X	Y	Z
8	3,529	L Fusiform Gynus		9.51	-34	-38	-18
9	2,013	L Cerebellum	Lobule IX (Hem)	7.99	-12	-52	-50
10	1,977	R Fusiform Gynus		6.04	34	-34	-20
11	1,315	L Cerebellum	Lobule VIIa Crus II (Hem)	5.75	-38	-70	-54
		L Cerebellum	Lobule VIIb (Hem)	3.22	-24	-72	-52

Table 2

Meta-analytical connectivity modelling

#	Vol (mm ³)	Macro	Cyto	z-score	MNI Coordinates		
					X	Y	Z
1	22,522	L dPMC		8.57	-26	4	60
		L SMA	Area 6	7.89	-2	12	54
		R SMA		7.51	6	22	46
2	12,497	L Inferior Parietal Lobule	hiP3	7.30	-30	-56	48
		L Precuneus	SPL (7P)	5.57	-12	-72	48
		L Inferior Parietal Lobule	hiP2	4.26	-46	-36	44
		L Inferior Parietal Lobule	Area 2	4.25	-44	-34	44
3	12,293	L Inferior Parietal Lobule	hiP1	3.56	-38	-44	44
		L vPMC	Area 44	6.27	-52	10	32
4	6,813	L Inferior Frontal Gyrus (p. Triangularis)		5.26	-44	32	20
		L Inferior Frontal Gyrus (p. Triangularis)	Area 45	4.80	-46	28	28
		R Angular Gyrus		6.41	34	-62	44
		R Middle Occipital Gyrus		5.51	32	-76	34
		R Superior Parietal Lobule	SPL (7P)	4.56	16	-68	52
5	6,307	R Precuneus	SPL (7A)	4.16	8	-60	50
		L Insula Lobe		6.95	-34	22	-4
		L Inferior Frontal Gyrus (p. Triangularis)	Area 44	4.03	-48	16	4
6	5,707	R dPMC		6.03	28	2	54
7	4,101	R vPMC		4.99	48	14	30
8	3,025	Right Inferior Frontal Gyrus (p. Orbitalis)		5.29	34	24	-10
9	1,745	Right Inferior Parietal Lobule	hiP2	4.56	42	-42	44
		Right Inferior Parietal Lobule	IPC (PF)	3.75	48	-40	48
10	1,739	Right Inferior Parietal Lobule	IPC (PFt)	3.67	50	-38	50
		Left Inferior Temporal Gyrus		5.43	-48	-62	-10

Table 3

Structural covariance connectivity

#	Vol (mm ³)	Macro	Cyto	t-score	MINI Coordinates		
					X	Y	Z
1	162,399	L dPMC		3.54	-47	9	32
		R dPMC		3.52	27	2	61
		R dPMC	Area 6	3.35	24	-12	63
		L SMA	Area 6	3.29	-1	-3	67
		R Inferior Frontal Gyrus (p. Triangularis)		3.24	48	36	27
		L Inferior Frontal Gyrus (p. Opercularis)		3.21	-43	21	33
2	10,584	R Middle Cingulate		3.16	3	-9	35
		R Cuneus	Area 18	2.29	6	-79	21
		L Cuneus		2.11	3	-78	30
		L Superior Occipital Gyrus	SPL (7P)	1.91	-9	-81	41
		L Cuneus	Area 17	1.90	-3	-84	17
		L Cuneus	Area 18	1.90	-1	-81	18
3	4,569	L Superior Temporal Gyrus		2.05	-57	-28	8
		L Superior Temporal Gyrus	OP 4	2.00	-60	-19	6
		L Superior Temporal Gyrus	TE 3	1.98	-61	-31	13
		L Middle Temporal Gyrus		1.94	-66	-42	8
		R S1	Area 3b	1.75	30	-37	57
		R S1	Area 2	1.73	30	-42	57
5	1,000	R Superior Occipital Gyrus		1.69	25	-88	27
		R Middle Occipital Gyrus		1.68	30	-87	24